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A new skink species of the genus *Sphenomorphus* Fitzinger, 1843 (Squamata, Scincidae) from Central Guangdong, South China

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Abstract

We collected nine specimens of the genus *Sphenomorphus* Fitzinger, 1843 (Squamata, Scincidae) from Liuxihe National Forest Park in central Guangdong, South China, which were found not to correspond to any currently recognized species. Here, we describe this new species, *Sphenomorphus lingnanensis* **sp. nov.**, integrating morphological and mitochondrial DNA (*COI* and *16S rRNA*) evidence. Phylogenetic analyses reveal the new species to be a sister taxon to *S. indicus* with uncorrected *p*-distances of 0.132 in *COI* and 0.021 in *16S rRNA*. The *p*-distance in *COI* between the new species and *S. indicus* exceeds that between *S. scutatus* and *S. solomonis* (0.057), and the *p*-distance in *16S rRNA* exceeds that between *S. cyanolaemus* and *S. sabanus* (0.005). Morphologically, this new species is distinguished from five congeners (including *S. indicus*) with comparable data by: (1) possessing 56–58 ventral scale rows (versus 65–69 in *S. indicus*); and (2) occupying a distinct position in the morphospace defined by the first two principal components derived from seven meristic variables. The description of *S. lingnanensis* **sp. nov.** raises the number of recognized *Sphenomorphus* species in China to nine. *Sphenomorphus lingnanensis* **sp. nov.** is currently known only from two proximate localities (approximately 5 km apart) in central Guangdong, where it is sympatric with the oviparous congener *S. incognitus*.

Key Words

Guangdong, mitochondrial DNA, morphology, new species, Scincidae, South China, *Sphenomorphus*, taxonomy

Introduction

The Scincidae represents one of the most species-rich and cosmopolitan families of squamate reptiles (Daza et al. 2024). Of the 1793 currently recognized scincid species (Uetz et al. 2025), 54 species across 11 genera are known to occur in China (Che et al. 2020; Cai et al. 2022; Qi et al. 2022a, b; Jia et al. 2023, 2024; Wang et al. 2024; Wang et al. 2025). These include 6 *Ablepharus*, 1 *Ateuchosaurus*, 1 *Emoia*, 4 *Eutropis*, 1 *Lygosoma*, 10 *Plestiodon*, 3 *Proto-blepharus*, 14 *Scincella*, 8 *Sphenomorphus*, 1 *Subdoluseps*, and 5 *Tropidophorus* species. Notably, nine of these Chinese species [*S. tonkinensis* (Nguyen et al. 2011), *Pl. takarai* (Kurita et al. 2017), *L. siamense* (Siler et al. 2018), *Pr. medogensis* and *Pr. nyingchiensis* (Che et al. 2020), *Sc. wangyuezhaoi* (Jia et al. 2023), *Sc. liangshanensis* (Jia et al. 2024), *T. vongx* (Wang et al. 2024), and *S. luelaiorum* (Wang et al. 2025)] have been described since 2011, indicating that more likely await discovery.

Scincids are distributed across most provinces and special administrative regions of China, including Taiwan, and are absent only from the northeastern provinces of Jilin and

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Heilongjiang. Within China, 12 scincid species across six genera have been recorded from Guangdong Province in the south, including *At. chinensis*, *Eu. longicaudata*, *Eu. multifasciata*, *Pl. chinensis*, *Pl. elegans*, *Pl. quadrilineatus*, *Sc. reevesii*, *S. incognitus*, *S. indicus*, *S. tonkinensis*, *T. hainanus*, and *T. sinicus* (Huang and Zhao 1999; Li et al. 2011; Rao et al. 2011; Cai et al. 2022). During field surveys to Guangdong-Hong Kong-Macao Greater Bay Area in May and July 2024, we collected nine specimens of the genus *Sphenomorphus* from Liuxihe National Forest Park (23.73°N, 113.84°E; Fig. 1) in central Guangdong. Additionally, two juveniles of the putative new species were observed in the nearby Nankunshan Provincial Nature Reserve (23.64° N, 113.85°E; Fig. 1). Careful examination of these specimens, combined with detailed morphological and phylogenetic comparisons to other recognized *Sphenomorphus* species, revealed substantial and consistent differences. These specimens could not be assigned to any known species and are therefore described herein as new to science.

Materials and methods

Animal collection and morphological examination

In May and July 2024, we collected nine specimens (five adults and four juveniles) from Liuxihe National Forest Park; additionally, we observed two juveniles of the same putative species in the nearby Nankunshan Provincial Nature Reserve (Fig. 1). All living specimens were transported to our laboratory at Wenzhou University and subsequently deposited as voucher specimens in the Research Center of Herpetology.

Morphological data were collected following the methods of Huang and Zhao (1999) and Grismer et al. (2019). Both mensural (measurements) and meristic (counts) characters were recorded for each of the nine specimens (Table 1). These data were collected to facilitate comparisons with previously published data for five other *Sphenomorphus* species mainly distributed in the Indo-China Peninsula and South China: *S. indicus* from the Wenzhou (WZ) and Shenzhen (SZ) populations, *S. incognitus* from the Liuxihe population, *S. preylangensis* from Vietnam (Grismer et al. 2019), *S. sungaicolus* from Malysia (Sumarli et al. 2016), and *S. tonkinensis* from the Hainan population (Suppl. material 1). The mensural data recorded included: snout-vent length (SVL), tail length, head length (from the posterior margin of the retroarticular process to the snout tip), head width (at the posterior end of the mandible), head height (at the deepest point), axilla-groin length (from the fore-limb to hind-limb insertion points), fore-limb length (from the insertion point of the fore-limb to the base of the fourth finger), and hind-limb length (from the insertion point of the hind-limb to the base of the fourth toe). Meristic data included counts of: prefrontals, supraoculars, loreals, temporals, supralabials, infralabials, midbody scale rows (counted transversely at midbody), ventral scale rows (counted along the abdominal midline from the gular fold), and subdigital lamellae of the fourth toe and finger.

DNA extraction, amplification, and sequencing

Total genomic DNA was extracted from tail muscle samples of all nine specimens (five adults and four juveniles) using Isolation Mini Kit (Nanjing, China) following the manufacturer's protocol. Primers for amplifying the mitochondrial cytochrome c oxidase subunit I (*COI*) and large subunit ribosomal RNA (*16S rRNA*) genes were designed using Vector NTI software (Lu and Moriyama 2004). The primer sequences were: *COI* F: 5'-CGG CAC CCT CTA CTT AAT CTT TGG-3', *COI* R: 5'-CCA TAG TAT TGC GGC GTC TCA TTT-3'; *16S rRNA* F: 5'-GCA CTT GTA

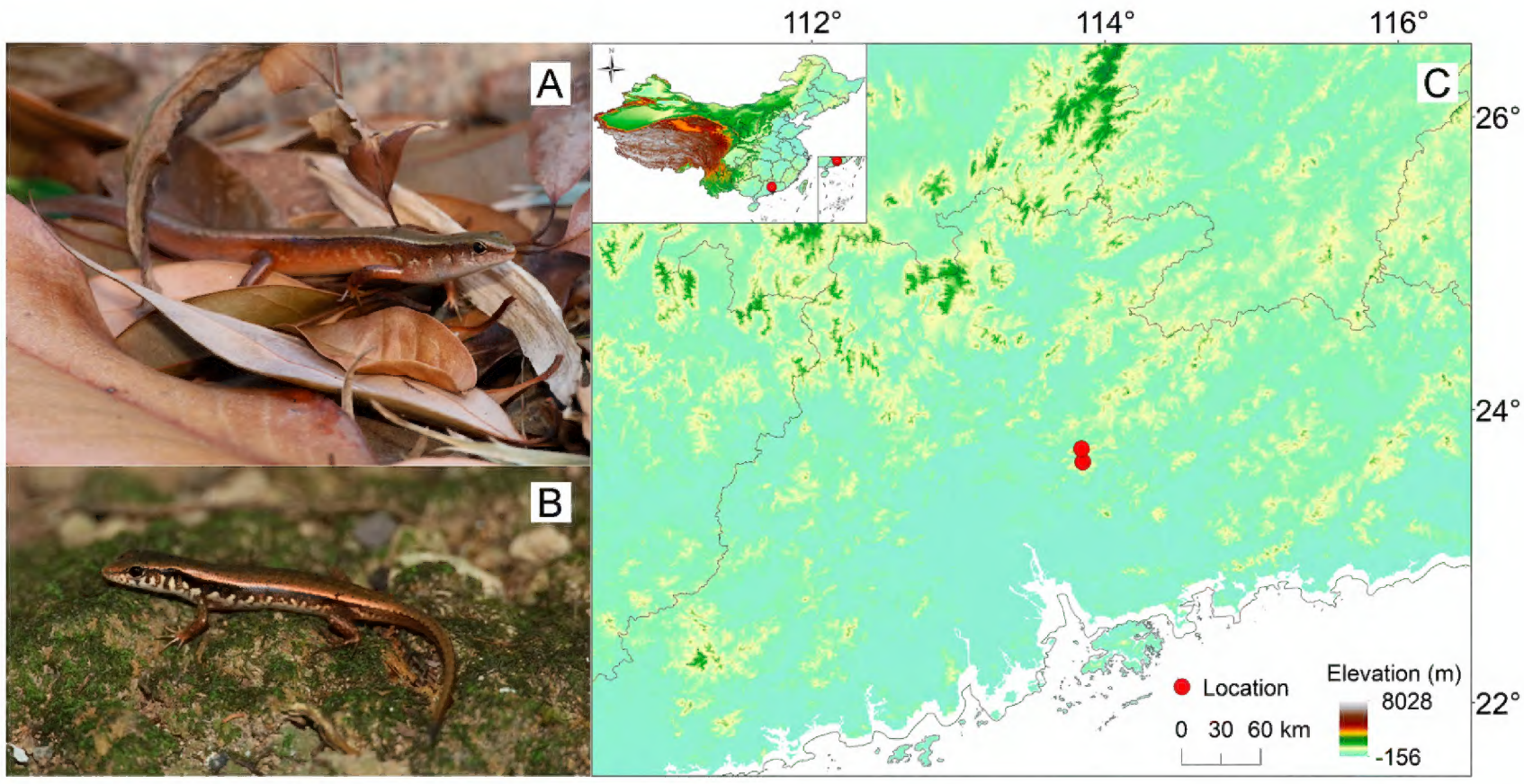

Figure 1. The adult female holotype (**A**, WZULXHTXSP1), a juvenile paratype of *S. lingnanensis* sp. nov. (**B**, WZULXHTXSP2), and two localities (**C**) in Central Guangdong where individuals of the new species were collected or witnessed.

Table 1. Mensural and meristic data for the type series of *Sphenomorphus lingnanensis* sp. nov. All length units are in mm.

	WZULXHTX								
	01 (FH)	**02 (JP)**	**03 (JP)**	**04 (JP)**	**05 (JP)**	**06 (FP)**	**07 (MP)**	**08 (MP)**	**09 (MP)**
SVL	75.8	32.5	34.3	36.0	59.3	54.9	59.0	79.5	77.4
Head length	16.2	9.7	9.8	10.2	13.1	12.7	13.0	16.8	16.2
Head width	9.4	5.1	5.8	5.7	7.6	7.7	8.5	10.1	10.3
Head height	8.1	4.0	4.5	4.41	6.6	5.2	5.2	7.2	7.3
Tail length	94.4	49.9	45.3*	54.0	84.5	93.2	67.0*	56.4*	113.7
Axilla-groin length	38.1	16.8	17.7	20.8	27.2	26.0	27.4	37.9	39.5
Fore-limb length	21.0	10.0	9.8	11.3	18.4	16.1	17.1	20.8	20.8
Fore-limb length	28.9	16.3	15.1	17.4	26.9	24.9	26.3	31.2	31.3
Prefrontals separation	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Supraoculars	4	4	4	4	4	4	4	4	4
Loreals	2	2	2	2	2	2	2	2	2
Temporals	4	4	4	4	4	4	4	4	4
Supralabials	7	7	7	7	7	7	7	7	7
Infralabials	7	7	7	7	7	7	7	7	7
Midbody scale rows	36	33	35	35	35	36	36	35	34
Ventral scale rows	57	57	56	58	58	56	56	56	56
4th toe lamellae	17	17	16	17	17	18	17	17	18
4th finger lamellae	10	10	11	11	10	10	11	12	11

* Regenerated tail.
FH: Adult female holotype; MP; Adult male paratype; JP: Juvenile paratype.

CCT TGC ATC ATG GGG-3', *16S rRNA* R: 5'-CTT GAA GAA GAT GGC GCT GTT ATC-3'. Polymerase chain reaction (PCR) amplifications were carried out in 30 µL volumes under the following thermal profiles: an initial denaturation at 94 °C for 3 min; 35 cycles of denaturation at 94 °C for 30 sec, annealing at 57.3 °C (*COI*) or 56.5 °C (*16S rRNA*) for 1 min, and extension at 72 °C for 2 min; followed by a final extension at 72 °C for 10 min. All reactions used Taq DNA polymerase (TaKaRa, Dalian, China) and were run on a Biometra Tone 96 thermal cycler (Jena, Germany). PCR products were purified and submitted for bidirectional Sanger sequencing to Tsingke Biotechnology Co., Ltd. (Beijing, China). The resulting forward and reverse sequences were assembled and edited to obtain consensus sequences for subsequent analyses.

Data analysis and phylogenetic reconstruction

Principal components analysis (PCA) was conducted using Statistica 14.0 (TIBCO Software Inc., USA) to visualize the morphological distinctness of the putative new species relative to five known congeners. The analysis was based on seven meristic variables: loreals, temporals, supralabials, infralabials, midbody scale rows, ventral scale rows, and lamellae under the fourth toe. Prior to multivariate analysis, mensural variables were standardized using Z-scores to remove the influence of scale differences.

Sequence chromatograms were assembled and edited using SeqMan within the Lasergene software suite (Burland 2000). Additional mitochondrial *COI* and/or *16S rRNA* gene sequences for 36 *Sphenomorphus* species and the outgroup *Tropidophorus hainanus* were downloaded from the NCBI GenBank database (accession numbers in Table 2). Sequences were aligned using the MUSCLE algorithm as implemented in MEGA6 (Tamura et al. 2013). The best-fit nucleotide substitution model was selected using PartitionFinder 2 (Lanfear et al. 2017). Bayesian inference (BI) phylogenies under the GTR+I+G model (5,000,000 generations and 25% burn-in) were then reconstructed for the *COI* and *16S rRNA* gene dataset using MrBayes 3.2.7a (Ronquist et al. 2012) within the PhyloSuite 1.2.2 platform (Zhang et al. 2020). Finally, pairwise uncorrected genetic (*p*) distances between selected pairs of *Sphenomorphus* species were calculated for each gene separately using MEGA6.

Results

The Bayesian Inference phylogenetic tree revealed a well-supported topology [Bayesian posterior probabilities (BPPs) ≥ 0.55 for most nodes; Fig. 2]. *Sphenomorphus lingnanensis* sp. nov. and *S. indicus* formed the closest sister group, with maximal support (BPP = 1; Fig. 2). The uncorrected *p*-distance between *S. lingnanensis* sp. nov. and *S. indicus* was 0.132 for *COI* and 0.021 for *16S rRNA*. These values substantially exceeded the minimum interspecific distances reported within the genus *Sphenomorphus*: 0.057 between *S. scutatus* and *S. solomonis* (*COI*), and 0.005 between *S. cyanolaemus* and *S. sabanus* (*16S rRNA*) (Suppl. material 2).

Morphologically, *S. lingnanensis* sp. nov. differed from *S. indicus* in two traits: (1) ventral scale rows numbered 56–58 in the new species versus 65–69 in *S. indicus*; and (2) *S. lingnanensis* sp. nov. occupied a distinct position within the morphospace defined by the first two axes of the PCA on seven meristic variables, largely or totally separating from *S. indicus* and other congeners (Fig. 3).

Table 2. NCBI GenBank accession numbers and localities of *Sphenomorphus* species used to perform molecular phylogenetic analysis.

	Species	Locality	GenBank numbers		References
			16S	***CO1***	
1	*S. acutus*	Philippine Archipelago	JF498079	NA	Linkem et al. 2011
2	*S. annamiticus*	Chum Noab, Koh Kong, Cambodia	MN414383	NA	Grismer et al. 2019
3	*S. apalpebratus*	Mawphlang, East Khasi Hills District, Meghalaya State, India	KF514651	NA	Datta-Roy et al. 2013
4	*S. buenloicus*	Buon Luoi, Gia Lai; Hon Ba NR., Khanh Hoa, Vietnam	HM773218	MH237969	Nguyen et al. 2011, 2018
5	*S. concinnatus*	Papua New Guinea	JF498080	NA	Linkem et al. 2011
6	*S. cranei*	Papua New Guinea	JF498082	NA	Linkem et al. 2011
7	*S. cryptotis*	Shangsi, Guangxi, China	OP942190	OP942215	Jia et al. 2023
8	*S. cyanolaemus*	Borneo	JF498084	NA	Linkem et al. 2011
9	*S. diwata*	Mindanao, Philippines	JF498086	NA	Linkem et al. 2011
10	*S. dussumieri*	NA	NA	MK089440	Unpublished
11	*S. fasciatus*	Philippine archipelago	JF498088	NA	Linkem et al. 2011
12	*S. incognitus*	Lingnan NR, Huangshan, Anhui, China	MH329292	MH329292	Tang et al. 2019a
13	*S. indicus*	Yixian, Huangshan, Anhui, China	MK450438	MK450438	Tang et al. 2019b
		Cixi, Zhejiang, China	OM117611	OM117611	Wu et al. 2022
14	*S. jobiensis*	Usino, Papua New Guinea	DQ915315	NA	Skinner 2007
15	*S. lingnanensis* **sp. nov.**	Liuxihe NFP, Guangdong, China (WZULXHTXSP1–5)	PQ249819-23	PQ252874–PQ252878	This study
16	*S. maculatus*	NA	MT609851	MT609543	Mulcahy et al. 2022
17	*S. maindroni*	NA	AY308311	NA	Unpublished
18	*S. melanopogon*	NA	AY308312	NA	Schmitz 2003
19	*S. muelleri*	NA	AY308313	NA	Schmitz 2003
20	*S. multisquamatus*	Borneo	JF498091	NA	Linkem et al. 2011
21	*S. phuquocensis*	Phu Ouoc Island, Kien Giang, Vietnam	MT523048	NA	Grismer et al. 2020
22	*S. praesignis*	Fraser's Hill, Pahang, Peninsular Malaysia	MN414387	NA	Grismer et al. 2019
23	*S. preylangensis*	Phnom Chi, Prey Lang, Kampong Thom, Cambodia	MN414388	NA	Grismer et al. 2019
24	*S. sabanus*	Borneo	JF498092	NA	Linkem et al. 2011
25	*S. sarasinorus*	NA	AY308315	NA	Schmitz 2003
26	*S. scutatus*	Papua New Guinea	JF498093	MH274670	Linkem et al. 2011; Mulcahy et al. 2022
27	*S. sheai*	NA	NA	PP931020	Unpublished
28	*S. simus*	NA	AY217967	NA	Schmitz 2003
29	*S. solomonis*	Papua New Guinea	JF498094	MH274678	Linkem et al. 2011; Mulcahy et al. 2022
30	*S. stellatus*	Kon Tum, Vietnam	HM773221	NA	Nguyen et al. 2011
31	*S. tersus*	Perlis, Malaysia	KX398015	NA	Sumarli et al. 2016
32	*S. tonkinensis*	Bac Me District, Ha Giang, Vietnam	OM387059	OM420330	Unpublished
33	*S. sungaicolus*	Hutan Lipur Sekayu, Terengganu, Malaysia	KX398013	NA	Sumarli et al. 2016
34	*S. valentinae*	Chu Yang Sin NP., Dak Lak, Vietnam	NA	PP931013	Bragin et al. 2025
35	*S. variegatus*	Philippine archipelago	JF498096	NA	Linkem et al. 2011
36	*S. yersini*	Hon Ba NR, Khanh Hoa, Vietnam	NA	MH237971	Nguyen et al. 2018
37	*T. hainanus*	Jinxiu, Guangxi, China	OM117612	OM117612	Wu et al. 2022

NA: Not available; NR: Natural Reserve; NFP: National Forest Park.

Taxonomy

Sphenomorphus lingnanensis sp. nov.

https://zoobank.org/3FCB1805-5CA9-4389-A71C-68818F250916

Figs 1, 4

Type materials. ***Holotype.*** • An adult female (WZULX-HTXSP1) collected on 7 May 2024 by Jun-Jie Zhong from Liuxihe National Forest Park (23.73°N, 113.84°E; altitude 460 m above sea level), Guangzhou City, Greater Bay Area, Guangdong Province, China.

Paratypes. • A series of juvenile paratypes (WZULX-HTXSP2–5) collected on 20 July 2024 by Jun-Jie Zhong and Kun Guo from the type locality.

Etymology. The specific epithet is the Latin adjective derived from the geographic term "Lingnan" in South China, denoting the region south of five mountain ranges, namely the Yuechengling, Dupangling, Mengzhuling, Qingtianling, and Dayuling.

Diagnosis. A medium-sized skink of the genus *Sphenomorphus* distinguished from its congeners by the following combination of morphological characters: Large, irregular white patches – often forming discontinuous vertical lines – extending from the postnasal region posteriorly to the hindlimbs; these markings are more conspicuous in juveniles and fade in adults. Dorsal and lateral scales smooth, cycloid. Prefrontals separated; parietals each bordered by a series of eight scales, the largest centrally, and in

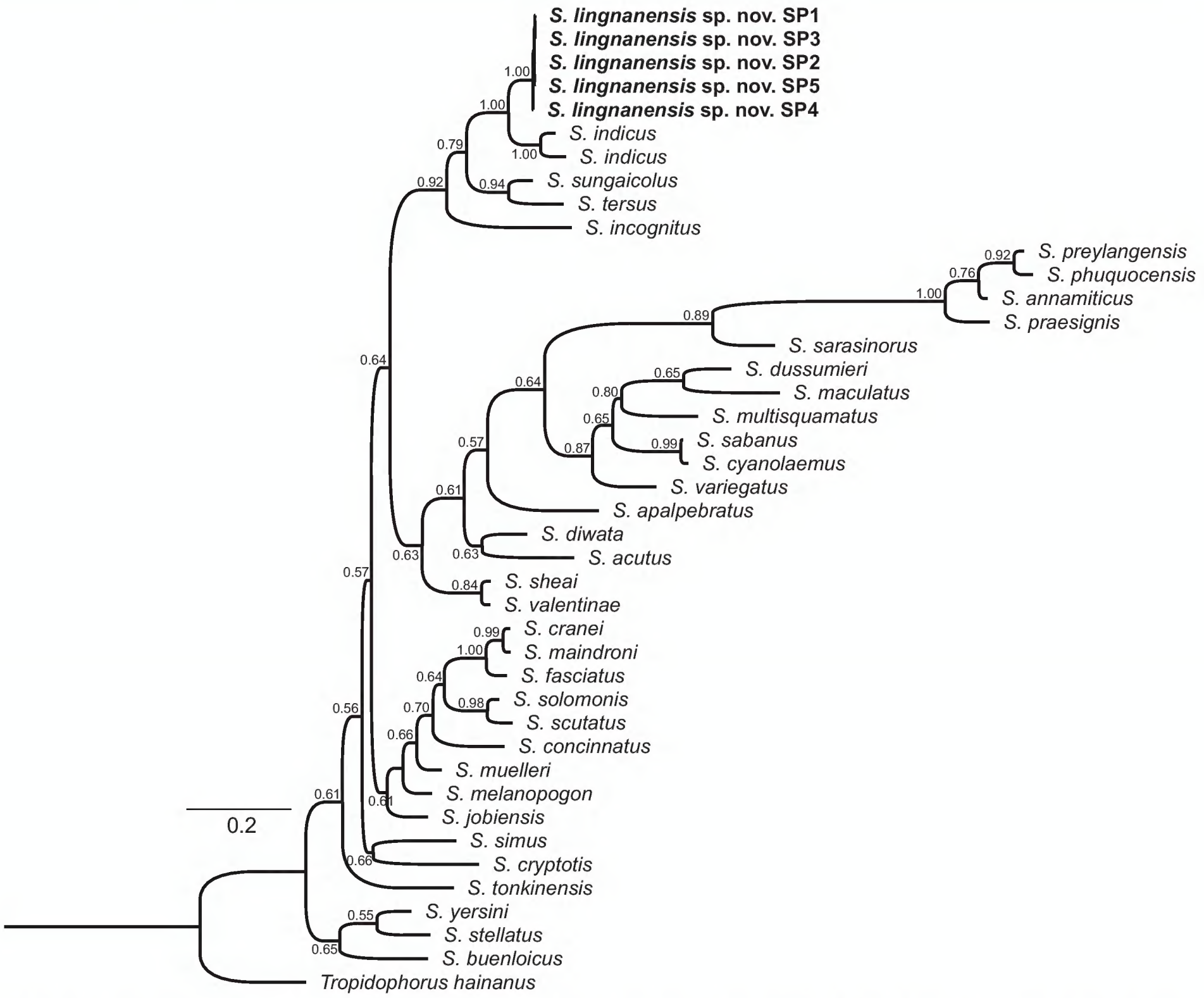

Figure 2. A phylogeny obtained by Bayesian Inference with higher posterior probabilities (≥ 0.55), showing phylogenetic relationships between *S. lingnanensis* sp. nov. and 35 other species of the genus *Sphenomorphus*.

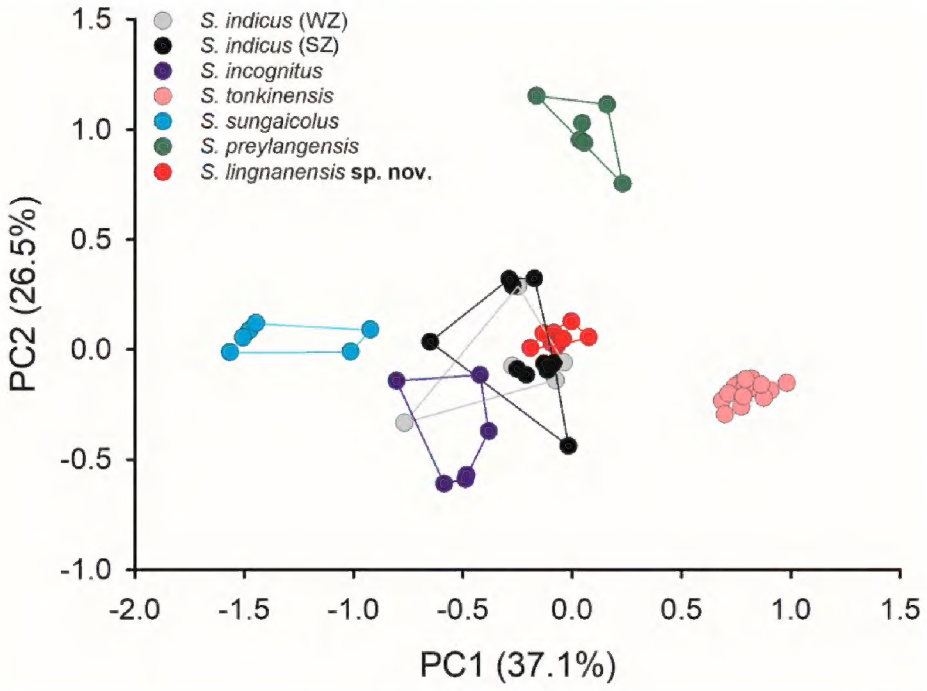

Figure 3. Positions of six *Sphenomorphus* species including *S. lingnanensis* sp. nov. on a two-dimensional plane defined by seven meristic morphological variables.

broad contact with the interparietal posteriorly; four nuchal scales; four supraoculars; two loreals, both in contact with supralabials; postnasal groove shallow or absent; supralabials seven; infralabials seven; chinshields in four pairs. Primary temporals two; secondary temporals two; the upper secondary temporals enlarged; subtemporals absent. Midbody scale counts 33–36; ventral scale counts 56–58; preanal scales two, enlarged. Subdigital lamellae under the fourth toe 16–18, under the fourth finger 10–12. Dorsum uniformly brown, occasionally with a few scattered small black spots; in juveniles, upralabials and infralabials bear distinct black or brown vertical stripes, which intensify in color from the snout posteriorly; in the holotype female, these labial scales become lighter in ground color.

Description of holotype. An adult female (Figs 1, 4A1–D1), with the following measurements (in mm): SVL 75.8, tail length 94.4, head length 16.2, head width 9.4, head height 8.1. Head moderate in size; snout slightly pointed. Dorsal and lateral scales ovate and imbricate; lateral scales near the abdomen and ventral scales approximately hexagonal. A single frontonasal scale (width greater than length) in contact laterally with the nasal and first loreal scales, and posteriorly with the prefrontal and frontal scales. Two prefrontal scales, each in contact with a loreal scale anterolaterally and a supraocular scale posterolaterally. A nearly triangular frontal scale, in contact laterally with the first and second supraocular scales and posteriorly with the frontoparietal scales.

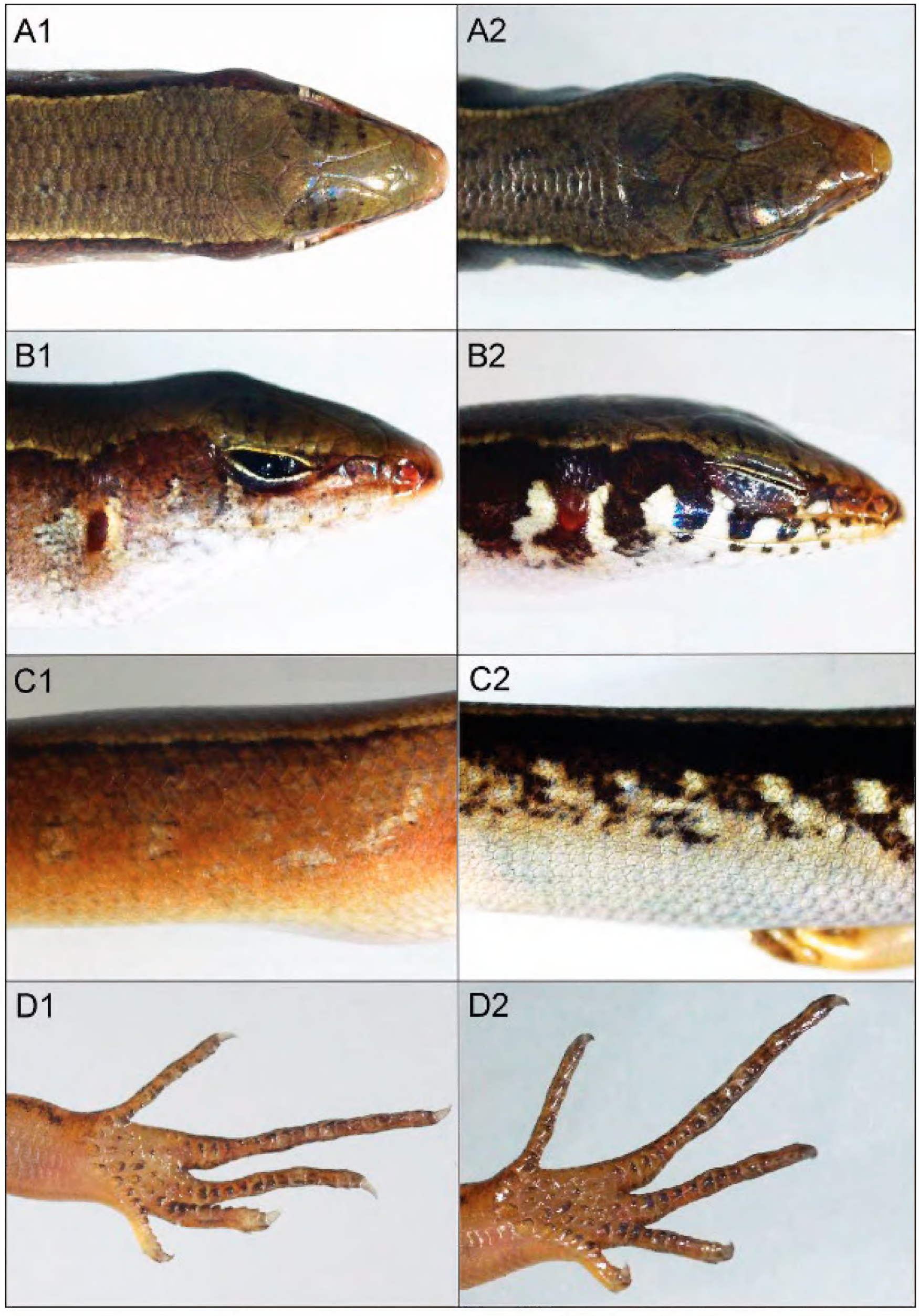

Figure 4. Close-up views of the adult female holotype (WZULXHTXSP1; left, from **A1–D1**) and a juvenile paratype (WZULXHTXSP3; right, from **A2–D2**) of *S. lingnanensis* sp. nov.

Four supraocular scales; the first and fourth subtriangular, and the second and third subtrapezoidal. Two frontoparietals, each in contact laterally with the third and fourth supraocular scales (and slightly with the second supraocular scale), and posteriorly with the parietal and interparietal scales. A nearly pentagonal interparietal scale, with

each side slightly curved and bearing a distinct eyespot. Large parietal scales, in contact posteriorly with the interparietal and frontoparietal scales, laterally with the upper secondary temporal scales, and posteriorly with the nuchal scales. Seven supralabial scales; the seventh was the largest, and the fifth was situated directly below the eye. Nostrils situated below the nasal scales. Nasal scales large, in contact ventrally with the first and second supralabial scales and posteriorly with the first loreal scale. The second loreal scale larger than the first, nearly rectangular in horizontal aspect, and in contact ventrally with the second and third supralabial scales and laterally with the first superciliary and frontonasal scales. Two preocular scales. Eight superciliary scales, not interrupted by the supraoculars. Two primary and two secondary temporals. Seven infralabials; the first was the smallest and the first two were in contact with the postmental scale. A large, semicircular mental scale, followed by a large postmental scale. Body scales smooth, dorsal scales similar in size to the vertebral scales. Two preanal scales, significantly enlarged compared to the ventral scales. Thirty-six longitudinal scale rows around midbody. Fifty-seven ventral scales. Subcaudal scales similar in size to the dorsal and caudal scales, but larger than the lateral caudal scales. Palmar and plantar scales rounded. A single row of supradigitals lamellae. Ten smooth subdigital lamellae under the fourth finger; 17 smooth subdigital lamellae under the fourth toe.

Coloration of holotype in life. The dorsal ground color was a bronzy brown over the head, body, limbs, and tail, grading from a darker reddish brown on the head to a pale bluish gray on the tail; the ventral surfaces of the head and body were pale yellow; the ventral ground color of the tail was lilac; and the ventral surfaces of the limbs were brown.

Color variation. In life, the coloration of the holotype (adult female) differed markedly from that of the paratypes (juveniles), as described above. In preservative, the dorsal ground color of the body becomes bluish gray, the dorsal surface of the head dark brown, and the ventral surfaces of the head and body white.

Distribution. *Sphenomorphus lingnanensis* sp. nov. is currently known only from the following two localities in central Guangdong Province, South China: Liuxihe National Forest Park and the nearby Nankunshan Provincial Nature Reserve, Guangzhou, within the Guangdong-Hong Kong-Macao Greater Bay Area. The two localities are separated by a straight-line distance of approximately 5 km.

Natural history. Based on current observations, *S. lingnanensis* sp. nov. inhabits evergreen broad-leaved forests at elevations between 440 and 600 m above sea level, typically in areas with a thick layer of leaf litter (Fig. 1). Individuals are often encountered along forest roadsides. When threatened, they retreat rapidly into the leaf litter. The species appears to be both diurnal and nocturnal.

Reproductive mode. *Sphenomorphus lingnanensis* sp. nov. is viviparous, as evidenced by a female (77.7 mm SVL) that produced a litter of four neonates on 13 August 2025. The postpartum body mass was 8.35 g, and neonate body masses ranged from 0.49 to 0.57 g (Table 3).

Table 3. Data on body mass and morphology of a female *S. lingnanensis* sp. nov. and 4 offspring to which it gave birth. All length units are in mm, and mass unit in g.

	Female	# Offspring			
		01	02	03	04
Body mass	8.35	0.49	0.55	0.54	0.57
Snout-vent length	77.7	28.5	30.1	30.3	30.9
Head length	16.4	8.9	8.8	9.1	8.8
Head width	10.6	5.00	5.3	5.1	5.6
Head height	8.2	3.74	4.2	4.0	4.1
Abdomen length	40.4	11.4	13.7	13.7	14.1
Tail length	70.2*	37.0	41.8	41.1	44.0
Fore-limb length	20.4	10.1	10.6	10.2	10.1
Hind-limb length	30.6	14.4	14.9	14.4	14.0
4th finger length	4.2	2.4	2.6	2.2	2.4
4th toe length	9.0	5.0	4.7	4.9	4.7

* Regenerated tail.

Discussion

Mitochodrial *COI* and/or *16S rRNA* sequence data have been available for 35 *Sphenomorphus* species (approximately 30% of all currently recognized taxa), including *S. lingnanensis* sp. nov. (Table 2). Our molecular phylogenetic analysis identifies *S. lingnanensis* sp. nov. as the sister taxon to *S. indicus* (Fig. 2). The substantial uncorrected *p*-distances (0.132 in *COI* and 0.021 in *16S rRNA*; Suppl. material 2) indicate considerable genetic divergence between *S. lingnanensis* sp. nov. and *S. indicus*. These distances exceed the minimum values reported for distinct species pairs within the genus *Sphenomorphus* (e.g., 0.057 in *COI* between *S. scutatus* and *S. solomonis*; 0.007 in *16S rRNA* between *S. cyanolaemus* and *S. sabanus*; Suppl. material 2), constituting robust evidence for the recognition of *S. lingnanensis* sp. nov. as a species distinct from its congeners, including *S. indicus*.

Morphological differences between *S. lingnanensis* sp. nov. and the five other congeneric species (including *S. indicus*) for which comparable data are available are also evident. This is demonstrated by the unique position occupied by *S. lingnanensis* sp. nov. in the morphospace defined by the first two principal components derived from seven meristic variables (Fig. 3). *Sphenomorphus lingnanensis* sp. nov. can be morphologically distinguished from *S. indicus* by its relatively narrower and more elongated head. Furthermore, ventral scale rows differ markedly between the two species, with non-overlapping ranges of 56–58 in *S. lingnanensis* sp. nov. versus 65–69 in *S. indicus*. The ventral scale count of *S. lingnanensis* sp. nov. further distinguishes it from other recently described congeners, such as *S. luelaiorum* (62–70; Wang et al. 2025), *S. valentinae* (52–56; Bragin et al. 2025), and *S. striatafaucium* (66; Quah and Grismer 2025).

Sphenomorphus is a species-rich genus of forest skinks distributed across Asia and the islands of the western Pacific (Uetz et al. 2025). Of the 116 currently recognized *Sphenomorphus* species, eight were previously known from China: *S. courcyanus*, *S. cryptotis*, *S. incognitus*,

S. indicus, *S. luelaiorum*, *S. maculatus*, *S. taiwanensis*, and *S. tonkinensis*. Among these, *S. taiwanensis* and *S. luelaiorum* are endemic to Taiwan (Huang and Zhao 1999; Darevsky et al. 2004; Nguyen et al. 2011, 2012; Qi et al. 2022a; Wang et al. 2025). The discovery of *S. lingnanensis* sp. nov. raises the total number of *Sphenomorphus* species in China to nine, four of which (*S. incognitus*, *S. indicus*, *S. tonkinensis*, and the new species) are now known from Guangdong Province. Our field observations indicate that *S. lingnanensis* sp. nov. is sympatric with *S. incognitus* but appears to be allopatric with respect to *S. indicus* and *S. tonkinensis* in the study region.

Despite its high species richness, the biology and ecology of the genus *Sphenomorphus* remain poorly studied. For example, while *Sphenomorphus* is recognized as a reproductively bimodal genus, the specific reproductive mode remains undocumented for a considerable number of species (Uetz et al. 2025). Among the nine *Sphenomorphus* species now known from China, *S. incognitus* (Ma et al. 2018) and *S. tonkinensis* (Du et al. 2023) are confirmed to be oviparous, whereas *S. indicus* (Ji et al. 2006) and *S. lingnanensis* sp. nov. (Table 3) are viviparous. The reproductive mode of the remaining five species is either unknown or unconfirmed. The phylogenetic pattern of reproductive mode in the genus *Sphenomorphus* is consistent with observations in other reproductively bimodal lizard genera [e.g., *Eremias* (Guo et al. 2011), *Trachylepis* (Weinell et al. 2019), *Phrynocephalus* (Guo and Wang 2007)] or populations [e.g., *Lerista bougainvillii* (Fairbairn et al. 1998; Adams et al. 2007), *Saiphos equalis* (Laird et al. 2019), *Zootoca vivipara* (Surget-Groba et al. 2006)], where congeners or conspecifics sharing the same reproductive mode typically cluster together. Therefore, the shared viviparity of *S. lingnanensis* sp. nov. and its sister species *S. indicus* aligns with this broader evolutionary trend. Future studies should aim to clarify the full distributional range, habitat preference, population status, diet, life history, and environmental adaptations of this newly described species.

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Supplementary material 1

Meristic data of the types series of *Sphenomorphus* species

Authors: Kun Guo, Jun-Jie Zhong, Yi-Peng Li, Wang Xu, Wei-Min Wang, Yu-Dong Li, Xin-Fan Yu, Xiang Ji

Data type: xlsx

Explanation note: Meristic data of the types series of *Sphenomorphus* species. See Material and Methods for abbreviations. Data on *S. tonkinensis*, *S. indicus*, *S. incognitus*, *S. lingnanensis* sp. nov. from China mainland; data on *S. sungaicolus* from Sumarli et al. 2016; data on *S. preylangensis* from Grismer et al. 2020.

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Link: https://doi.org/10.3897/zse.102.183764.suppl1

Supplementary material 2

Mean group distance of p-distance between Sphenomorphus

Authors: Kun Guo, Jun-Jie Zhong, Yi-Peng Li, Wang Xu, Wei-Min Wang, Yu-Dong Li, Xin-Fan Yu, Xiang Ji

Data type: xlsx

Explanation note: Mean group distance of p-distance between Sphenomorphus (CO1: Upper-right\16S: Lower-left). Only take the first three letters of the specific epithet in the Latin binomial name.

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